



This figure displays a sequence alignment of the TGFBR1 gene across multiple species and isoforms. The alignment is presented in a grid format with the amino acid positions on the x-axis and the different sequences on the y-axis. Each cell in the grid contains a single amino acid residue, colored according to its hydrophilicity: red for hydrophobic (P, I, M, V, L, F, Y, W) and green for hydrophilic (A, C, D, E, G, H, K, N, Q, S, T). A color bar at the bottom provides a key for these colors.

The alignment highlights regions of high conservation (green) and divergence (red). Key functional domains, such as the extracellular receptor domain, transmembrane domain, and intracellular kinase domain, are visible. The alignment also includes several isoforms (e.g., i1, i2, i3, i4, i5, i6, i7, i8, i9, i10, i11, i12, i13, i14, i15, i16, i17, i18, i19, i20, i21, i22, i23, i24, i25, i26, i27, i28, i29, i30, i31, i32, i33, i34, i35, i36, i37, i38, i39, i40, i41, i42, i43, i44, i45, i46, i47, i48, i49, i50, i51, i52, i53, i54, i55, i56, i57, i58, i59, i60, i61, i62, i63, i64, i65, i66, i67, i68, i69, i70, i71, i72, i73, i74, i75, i76, i77, i78, i79, i80, i81, i82, i83, i84, i85, i86, i87, i88, i89, i90, i91, i92, i93, i94, i95, i96, i97, i98, i99, i100, i101, i102, i103, i104, i105, i106, i107, i108, i109, i110, i111, i112, i113, i114, i115, i116, i117, i118, i119, i120, i121, i122, i123, i124, i125, i126, i127, i128, i129, i130, i131, i132, i133, i134, i135, i136, i137, i138, i139, i140, i141, i142, i143, i144, i145, i146, i147, i148, i149, i150, i151, i152, i153, i154, i155, i156, i157, i158, i159, i160).

